Designation	Species	Epitope	Western Blot	IHC	FACS	Epitope sequence
29C11	rabbit	Pro2	Yes	yes**	n.d.	IDELKECFLNQTDETLSNVE
31A5	rabbit	Pro3	Yes	yes**	yes	ELLQEFIDDNATTNAIDELK
6A1	rabbit	Pro2-3	Yes	n.d.	no	TTNAIDELKECFLNQ
14A12	rabbit	Pro3	Yes	n.d.	yes	ELLQEFIDDNATTNAIDELK
6B12	rabbit	Pro3	Yes	n.d.	yes	ELLQEFIDDNATTNAIDELK
2D3	rabbit	Pro5	Yes	n.d.	yes	SQHCYAGSGCPLLENVISKTI
16D8	rabbit	Pro3	Yes	n.d.	yes	ELLQEFIDDNATTNAIDELK
31-1H7	mouse	n.d.	Yes	n.d.	yes	
197-1H11	mouse	Pro5	Yes	n.d.	no	SQHCYAGSGCPLLENVISKTI
32-1G11	mouse	n.d.	Yes	n.d.	yes	
304-1A5	mouse	n.d.	Yes	n.d.	yes	
98-1F4	mouse	n.d.	Yes	n.d.	no	

Fig. 1A

pc.h.mam.6a1.cell-57.579.1.t7

CACCATGGAGACAGGCCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCA
GTCGCTGGAGGAGTCCGGCGGTCGCCTGGTAACGCCTGGAGGATCCCTGACACTCACCTGCAC
AGTCTCTGGAATCGACCTCAGTAGCTATGGAGTGGGCTGGGTCCGCCAGGCTCCAGGGAAGG
GGCTGGAATACATCGGAATCATTAGTAAAATTGATAACACATACTACGCGAACTGGGCGAAA
GGCCGATTCACCATCTCCAAAACCTCGTCGACCACGGTGGATCTGAAAATGACCAGTCTGACA
ACCGAGGACACGGCCACCTATTTCTGTACCAGAGGGTCTTTTGATCCCTGGGGCCCAGGCACC
CTGGTCACCGTCTCCTCAGGGCAACCTAA

pc.h.mam.16d8.cell-22.394.1.t7

CACCATGGAGACAGGCCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCA
GTCGGTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCAC
AGTCTCTGGATTCTCCCTCAGCAGCTACGACATGACCTGGGTCCGCCAGGCTCCAGGGAAGGG
GCTGGAATGGATCGGAACCATTAGTACTATTGGTAGCCCATTTTACGCGAGCTGGGCGAGAGG
CCGATTCACCATCTCCAAAACCTCGACCACGGTGGATCTGAAAATCACCAATCCGACAACCGA
GGACACGGCCACGTATTTTTGCGGCAGATTTCGGATTGCTGGTGA TGGTGCCTTCTGGGGCCC
AGGCACGCTGGTCACCGTCTCCTCAGGGCAACCTAA

pc.h.mam.16d8.cell-21.393.2.t7

CACCATGGAGACAGGCCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCA
GTCGGTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTAGGACACCCCTGACACTCACCTGCAC
AGTCTCTGGATTCTCCCTCAGCAGCTACGACATGACCTGGGTCCGCCAGGCTCCAGGGAAGGG
GCTGGAATGGATCGGAACCATTAGTACTATTGGTAGCCCATTTTACGCGACCTGGGCGAGAGG
CCGATTCACCATCTCCAAAACCTCGACCACGGTGGATCTGAAAATCACCAATCCGACAACCGA
GGACACGGCCACGTATTTTTGCGGCAGATTTCGGATTGCTGGTGATGGTGCCTTCTGGGGCCC
AGGCACGCTGGTCACCGTCTCCTCAGGGCAACCTAA

pc.h.mam.6b12.cell-19.339.4.t7

CACCATGGAGACAGGCCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCGGTGTCA
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AGTCTCTGGAATCGACCTCAGCACCTACGACATGACCTGGGTCCGCCAGGCTCCAGGGAAGG
GACTGGAATGGATCGGAACCATTAGTACTCTTGGTACCCCTTTTTCCGCCAATTGGGCGAGAG
GCCGATTCACCATCTCCAAGACCTCGACCACGGTGGATCTGAAAATCGCCAGTCCGACGACCG
AAGACACTGCCACATATTTTTGTGGCAGATTGCGGATTGCTCATGATGGTGCCTTCTGGGGCC
CAGGCACGCTGGTCACCGTCTCCTCAGGGCAACCTAA

Fig. 1B

pc.h.mam.2d3.cell-65.576.1.t7

CCCATGGAGACAGGCCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAG
GAGCAGCTGAAGGAGTCCGGAGGAGGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTG
CACAGTGTCTGGAATCGACCTCAATATCGATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGA
AGGGGCTGGAATGGATCGGAATTATTGGTACTCGTGGTGGCACATGGTTCGCGAGCTGGGCG
AAAGGCCGATTCACCATCTCCAAAACCCCGACCACAGTGGATCTGAAAATCCCCAGTCCGAC
AACCGAGGACACGGCCACCTATTTCTGTGCCAGTATCTATTCTGATAGTGGTACTTATACGAC
CTTGTGGGGCCCAGGCACCCCGGTCACCGTCTCCTCAGGGCAACCTAA

pc.h.mam.14a12.cell-3.333.1.t7

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CGTCTCTGGATTCTCCCTCAGCAGCGTCGACATGACCTGGGTCCGCCAGGCTCCAGGGAAGGG
GCTGGAATGGATCGGAACCATTAGTACTCGTAGTAGCACATACTACGCGAGCTGGGCGAAAG
GCCGATTCACCATCTCCAAAACCTCGACCACGGTGGATCTGAAAATCACCAGTCCGACAACCG
AGGACACGGCCACGTATTTCTGTGGCAGATTTCGGATTGCTGGTGATGGTGCCTTCTGGGGCC
CAGGCACGCTGGTCACCGTCTCCTCAGGGCAACCTAA

pcr.g.mam.29c11.c211.11779.780com

GGAAGGCTGCGCTGGCTTTTCCTGGTCGCTGTGCTCAGAGGTGTCCAGTGTCAGTCGCTGGAG
GAGTCCGGGGGTNGCCTGGTAACGCCTGGGACACCCCTGANANTCACCTGCACAGCCTTTGG
ATTTTCCCTCAGTAGCTGGTCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATG
GATCGGAATGATTGGTATTGTTGGTAGTGGCACATAATANGCGACCTGGGCGAAAGGCCGAT
TCACCATTTCCAAAACCTTGTGACCACGGTCGATTTGAAAATGACCAGTTTGACAACCGAGGA
CACGGCCACCTATTTTTGTGTCAGAGGGGGTAGTTTTANTTTTGCTACCGCCTTGTGGGGCCCA
GGCACCCTGGTCACCGTNTCCTCAGGGCAACCTAA

pcr.g.mam.31a5.c178.11884.780 com

TTGCAGGCTGCGTGGTTTTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGTCGGTGGAGG
AGTCCGGGGGGTNGCCTGGTAACNCCTGGGACACCCCTGACANTTTTTTGCAAAGTNTTTGGAT
TTTCCCTCAGCAGNTACGANATGACCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATGG
ATNGGAACCATTAGTANTTGTGGTAATGGATAATACGCGACCTGGGCGAAAGGCCGATTCAC
CATTTCCAAAACCTTGACCACCGTGGATTTGAAAATCACCAGTCCGACAACCGAGGACACGG
CCAAGTATTTTTGTGGCAGATTTCGGATTGCTGGTGATGGTGCTTTTGGGGCCCGGGCACGCT
GGTCACCGTNTCCTCAGGGCAACCTAA

Fig. 1C

Pro-1 MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

Pro-2 MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

Pro-3 MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

Pro-4 MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

Pro-5 MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

Pro-7 MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

Pro-8 MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

Pro-9 MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

Glob-2 MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

Pro-20 MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

N-terminal recombinant GSGMKETAAAKFERQHMDSPDLGTDDDDKAMAISDPNS.....HCYAGSGCPLLENVISK

Peptide with Enterokinase and Thrombin cleavage sites — Mammaglobin sequence

Fig. 2

Reactivity of Mouse Monoclonal antibodies to Mammaglobin with peptides and recombinants											
Antibody	Pro2	Pro-3	Pro-4	Pro-5	Pro-6	Pro-7	Pro-8	Glob-2	amma+Tlinal	recon	TRX
31-1H7	0.065	0 059	0.059	0.061	0.06	0.066	0.07	0.063	2.788	0.074	0.116
32-1G11	0.056	0.055	0.054	0.054	0.055	0.057	0.055	0.055	2.75	0.057	0.07
197-1H11	0.055	0.054	0.053	1.139	0.054	0.055	0.055	0.055	2.502	2.596	0.064
304-1A5	0.054	0.054	0.053	0.053	0.054	0.053	0.053	0.054	2.7	0.056	0.064
98-1F4	0.068	0.055	0.053	0.055	0.059	0.064	0.11	0.112	2.819	0.118	0.121
967	0.055	0.057	0.056	0.056	0.055	0.62	0.056	0.637	1.566	0.069	0.159
Blank	0.056	0.055	0.053	0.055	0.052	0.053	0.053	0.053	0.056	0.052	0.06

Fig. 3A

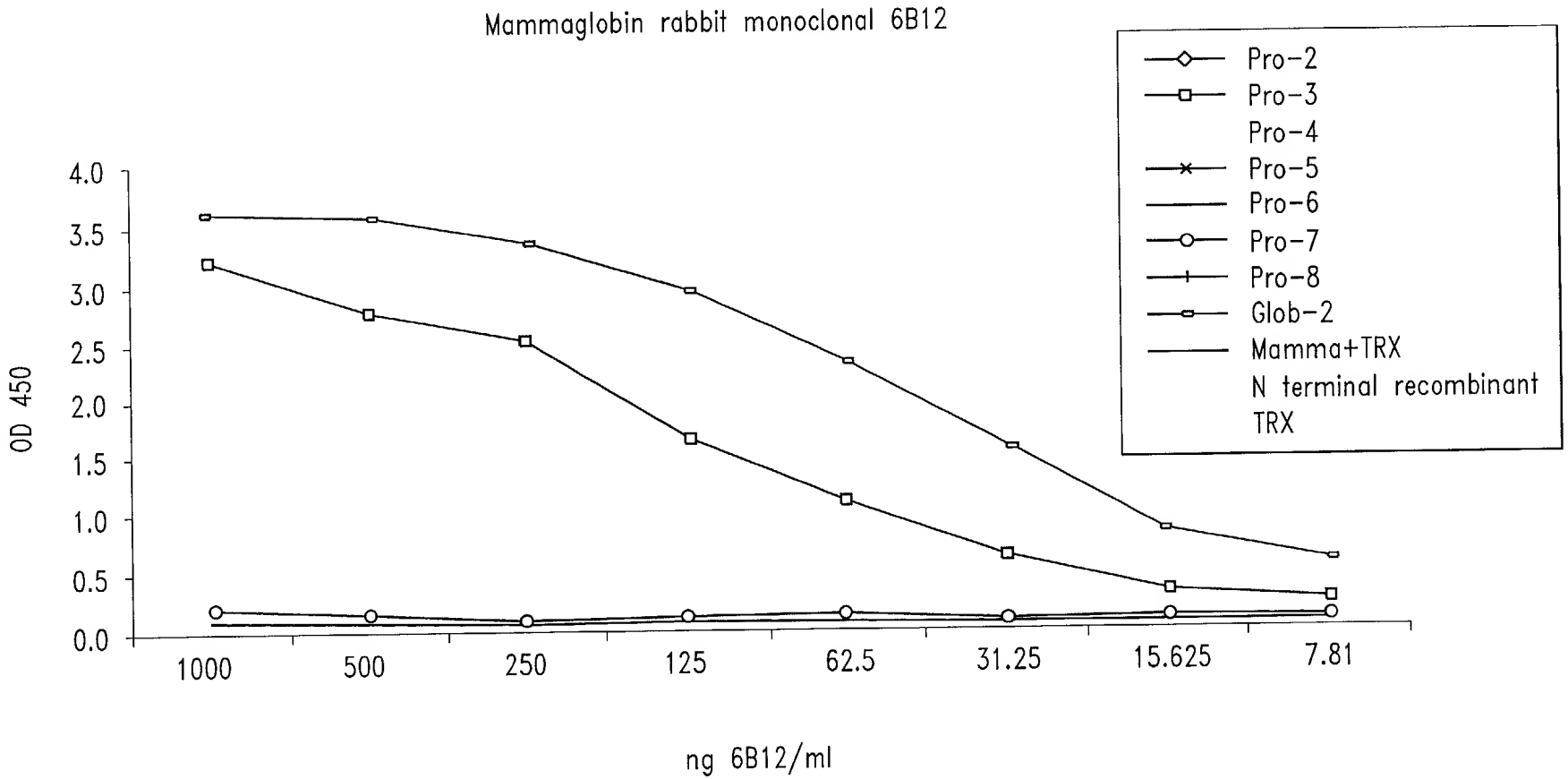

Mammaglobin rabbit monoclonal 6B12
Pro-2
Pro-3
Pro-4
Pro-5
Pro-6
Pro-7
Pro-8
Glob-2
Mamma+TRX
N terminal recombinant TRX
OD 450
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
1000
500
250
125
62.5
31.25
15.625
7.81
ng 6B12/ml

Fig. 3B

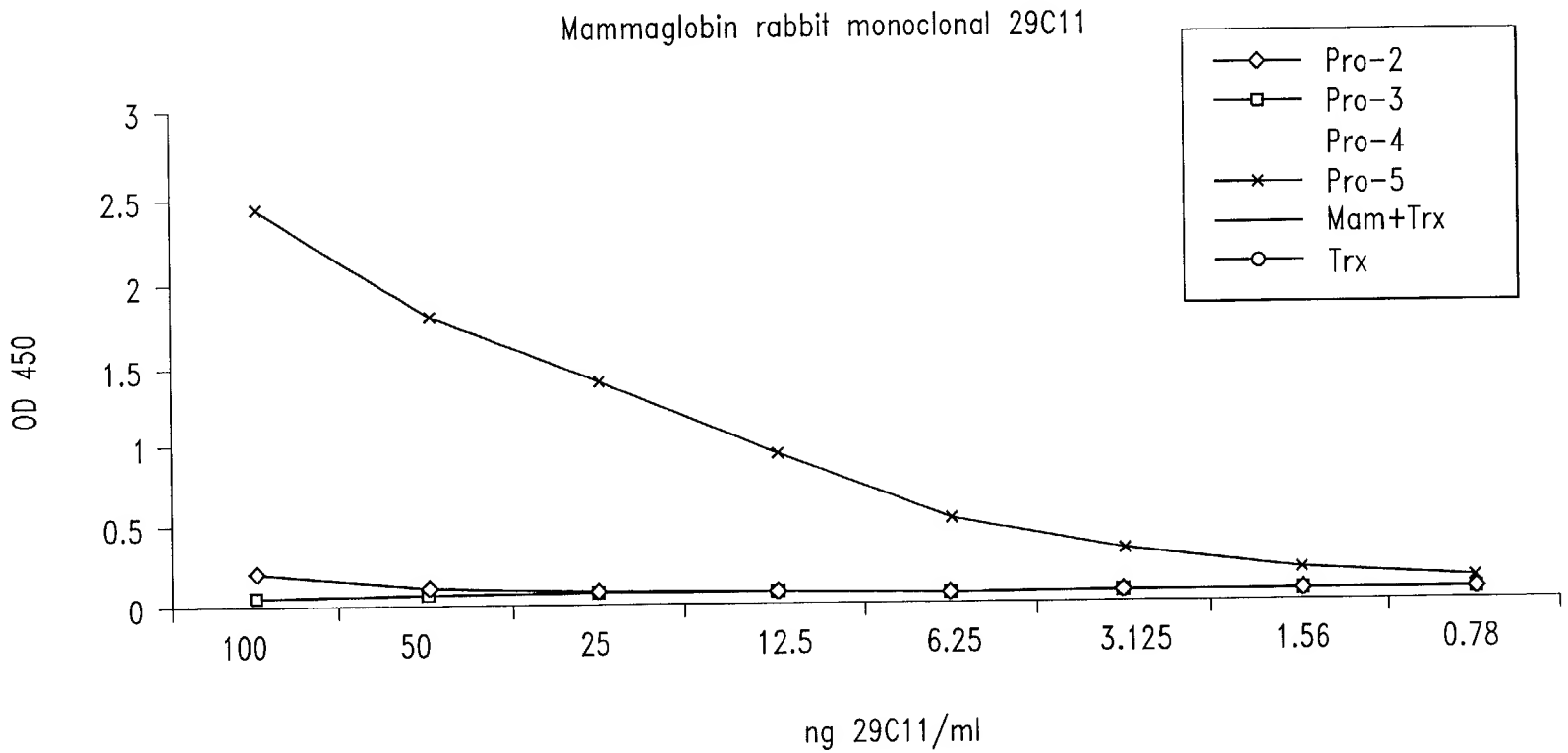

Mammaglobin rabbit monoclonal 29C11
Pro-2
Pro-3
Pro-4
Pro-5
Mam+Trx
Trx
OD 450
3
2.5
2
1.5
1
0.5
0
100
50
25
12.5
6.25
3.125
1.56
0.78
ng 29C11/ml

Fig. 3C

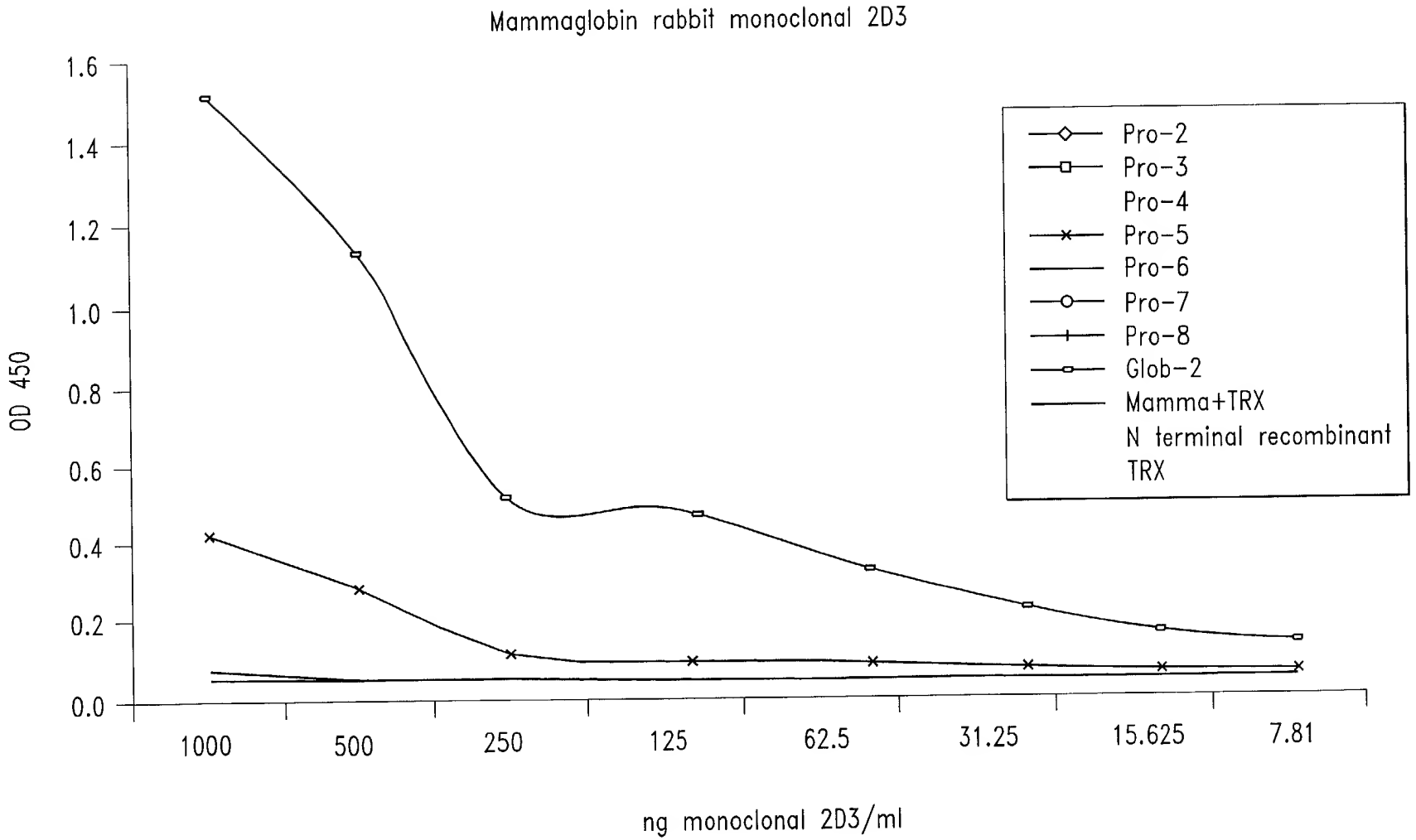


Fig. 3D

Staining of permeabilized human breast tumor cell line MDA-MB415 with rabbit anti-mammaglobin monoclonal antibodies

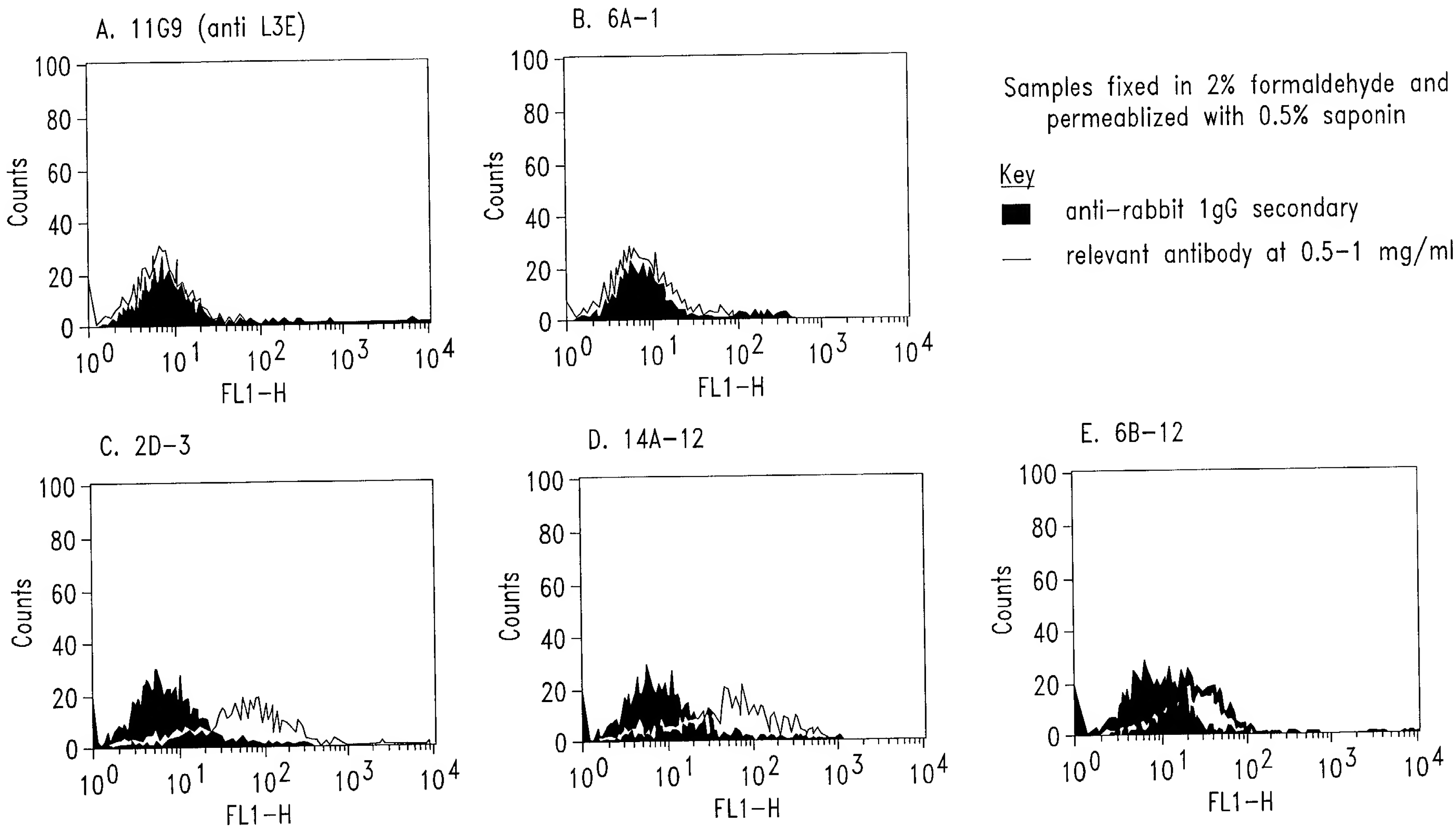


Fig. 4A

Staining of permeabilized human breast tumor cell lines with murine anti-mammaglobin monoclonal antibodies

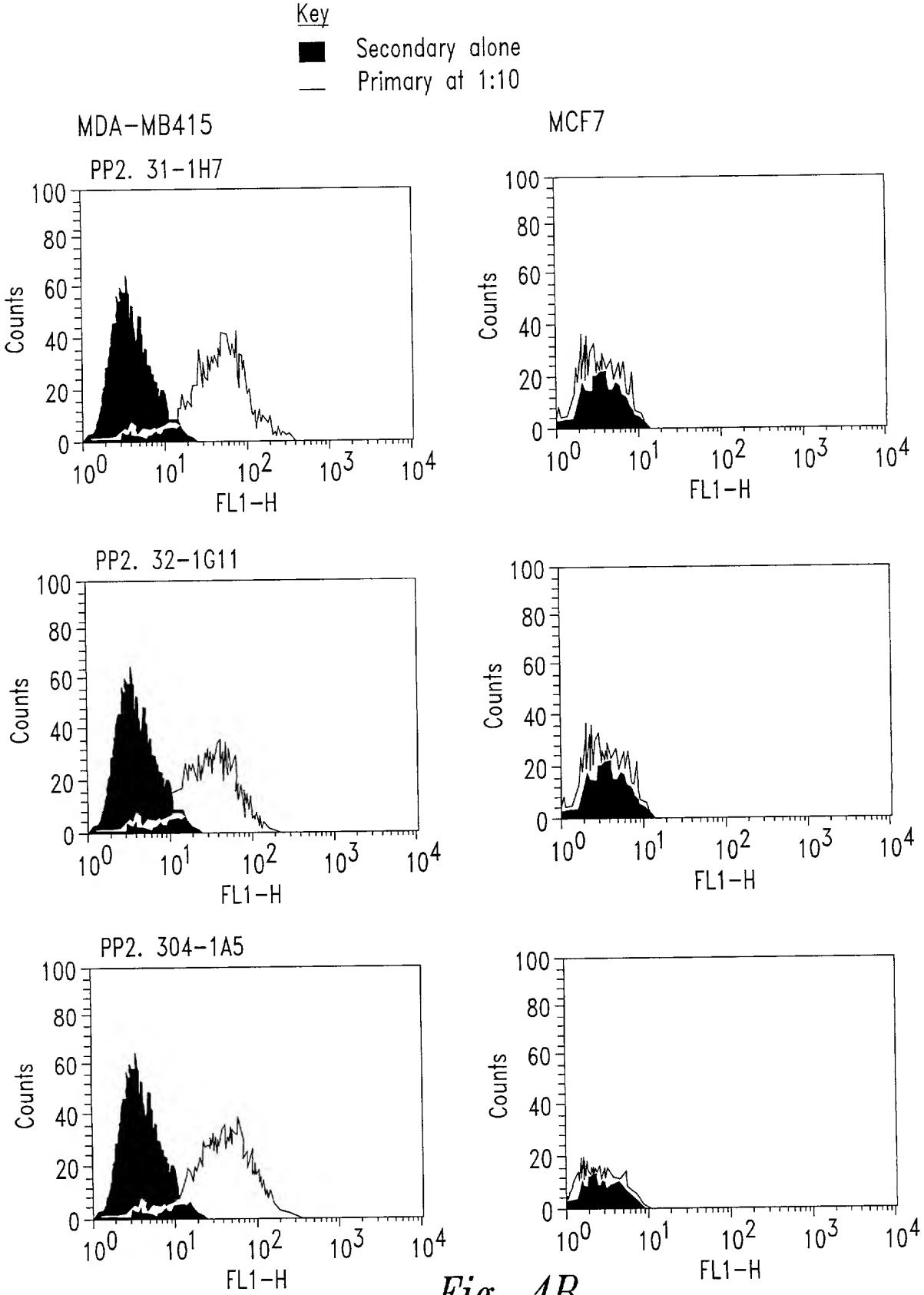
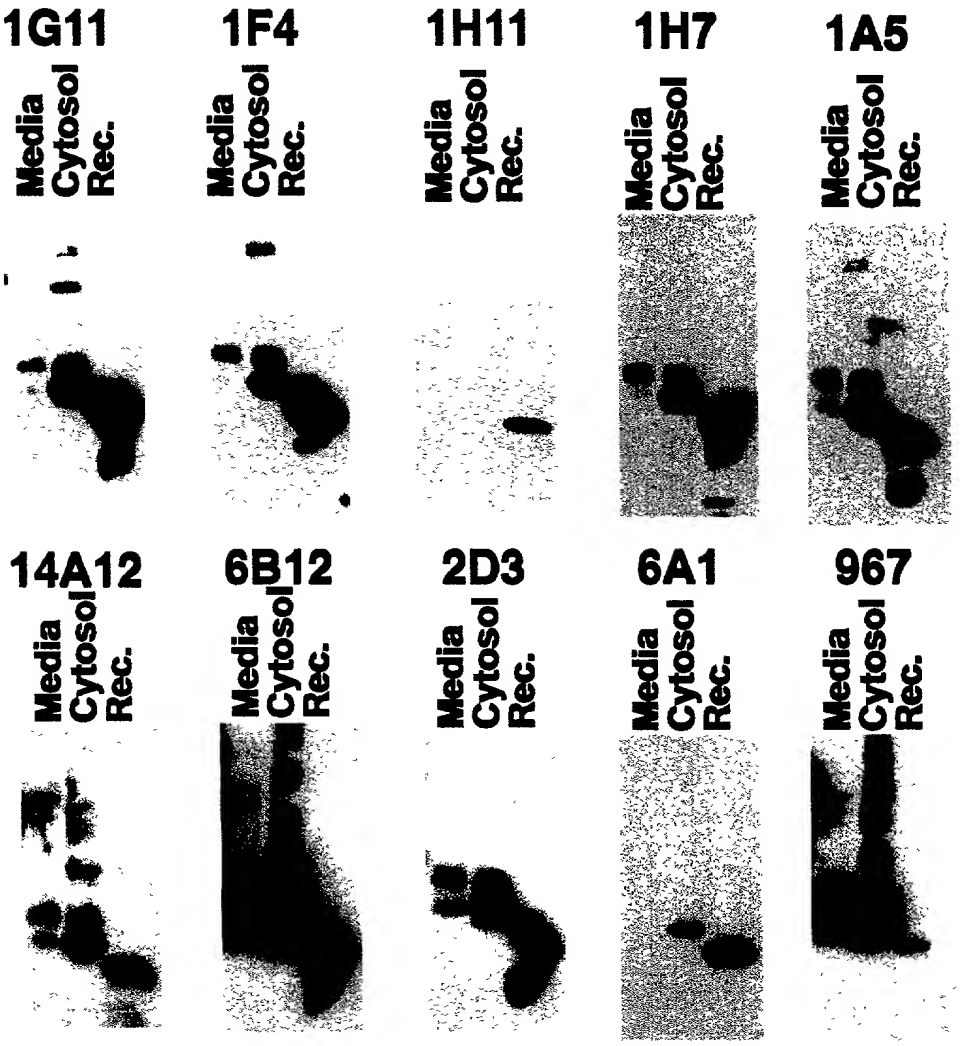


Fig. 4B

Western blot analysis of Mammaglobin from MB415 cells



Mouse monoclonal: 1G11, 1F4, 1H11,1H7, 1A5
Rabbit monoclonal: 14A12, 6B12, 2D3, 6A1
Rabbit polyclonal: 967

Rec.: bacterially expressed recombinant mammaglobin

Fig. 5

IHC analysis of mammaglobin expression in normal tissue.

Normal Tissue	Mam-29C11/31A5
Breast	3-
Adrenal	0
Cervix	0
Colon	0
Duodenum	0
Gall bladder	0
Ileum	0
Kidney	0
Ovary	0
Pancreas	0
Paroud gland	0
Prostate	0
Skeletal muscle	0
Spleen	0
Testis	0

Fig. 6

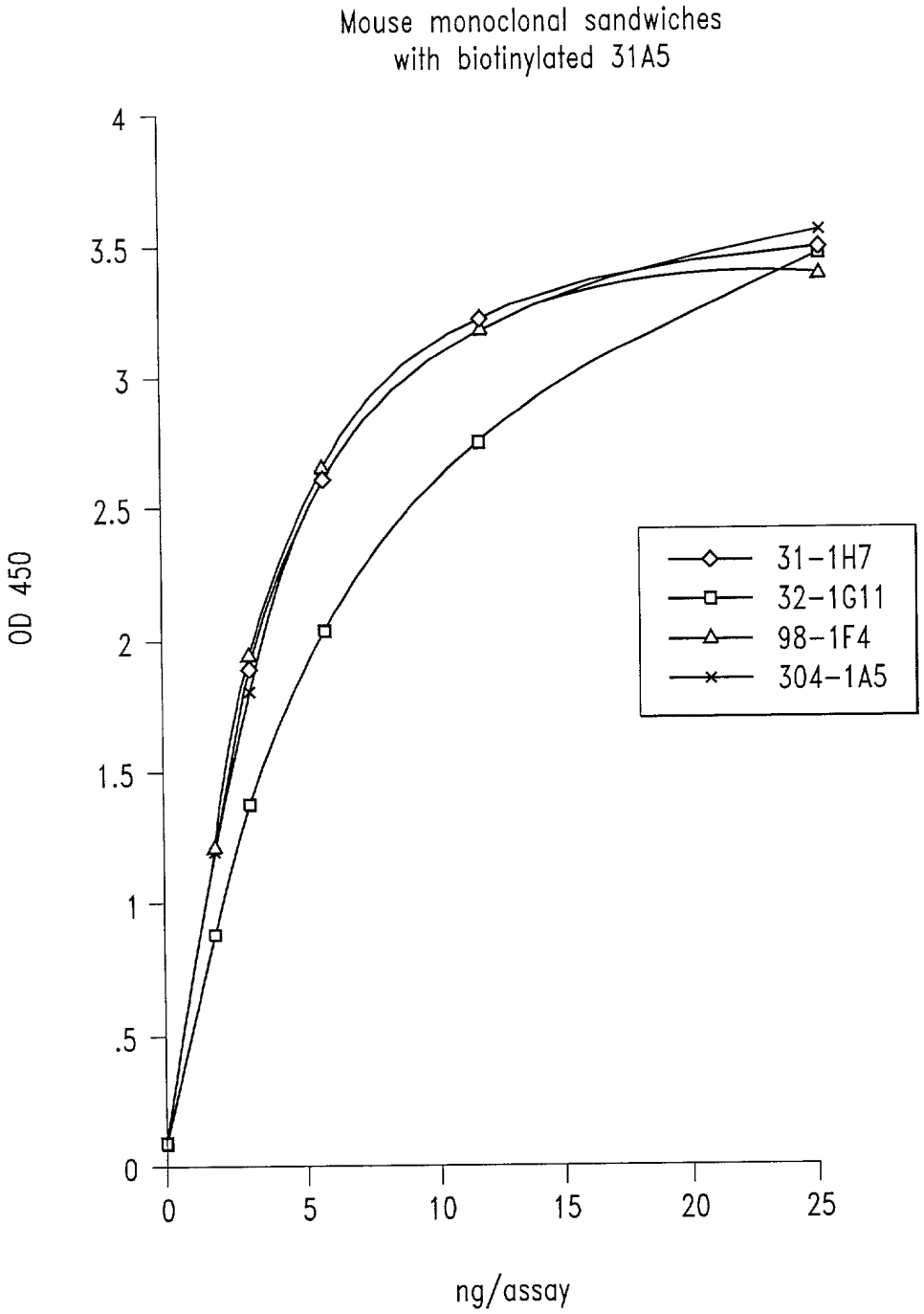

Mouse monoclonal sandwiches
with biotinylated 31A5
OD 450
4
3.5
3
2.5
2
1.5
1
.5
0
0
5
10
15
20
25
ng/assay
31-1H7
32-1G11
98-1F4
304-1A5

Fig. 7A

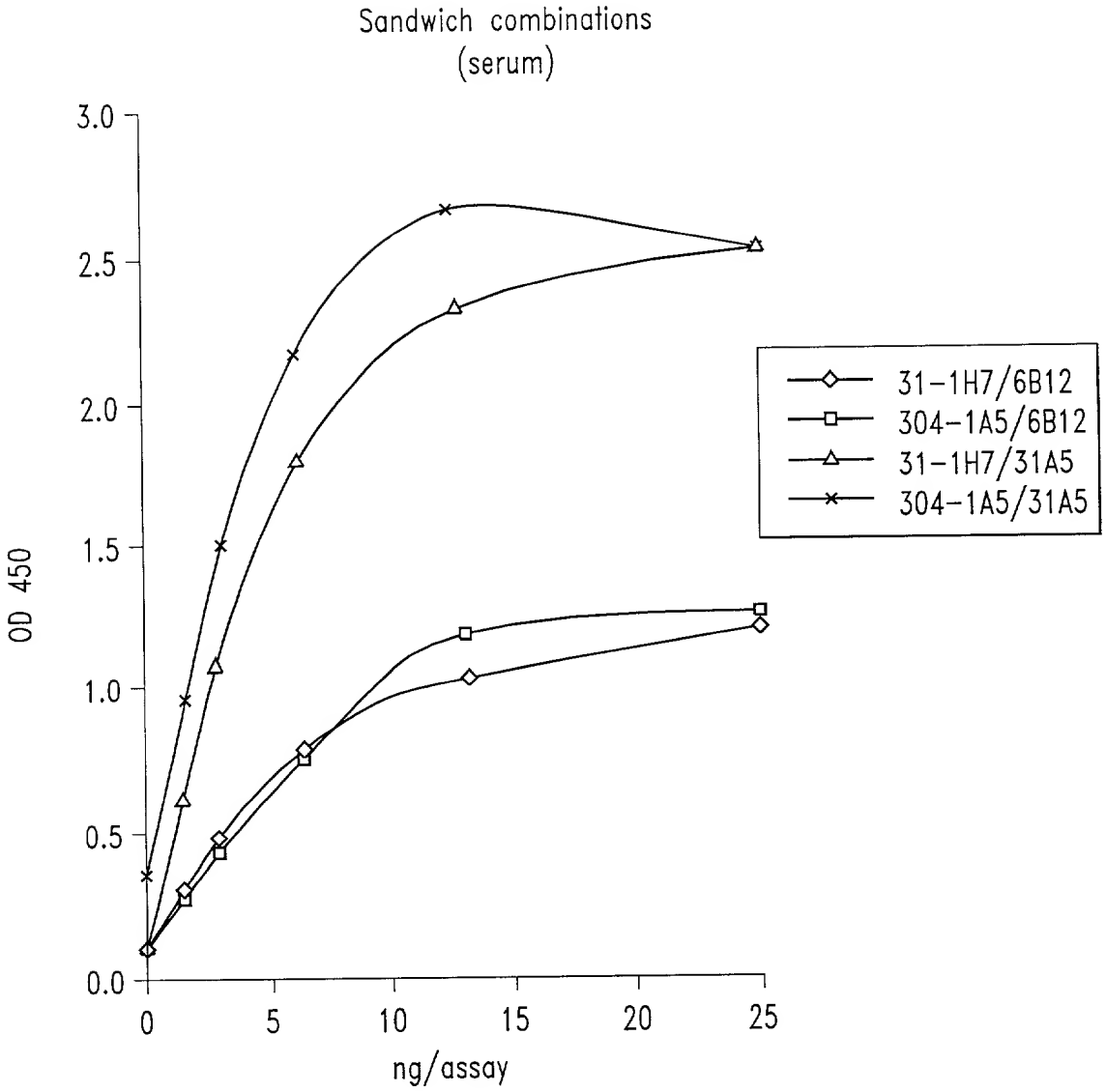

Sandwich combinations
(serum)
3.0
2.5
2.0
1.5
1.0
0.5
0.0
OD 450
0
5
10
15
20
25
ng/assay
31-1H7/6B12
304-1A5/6B12
31-1H7/31A5
304-1A5/31A5

Fig. 7B

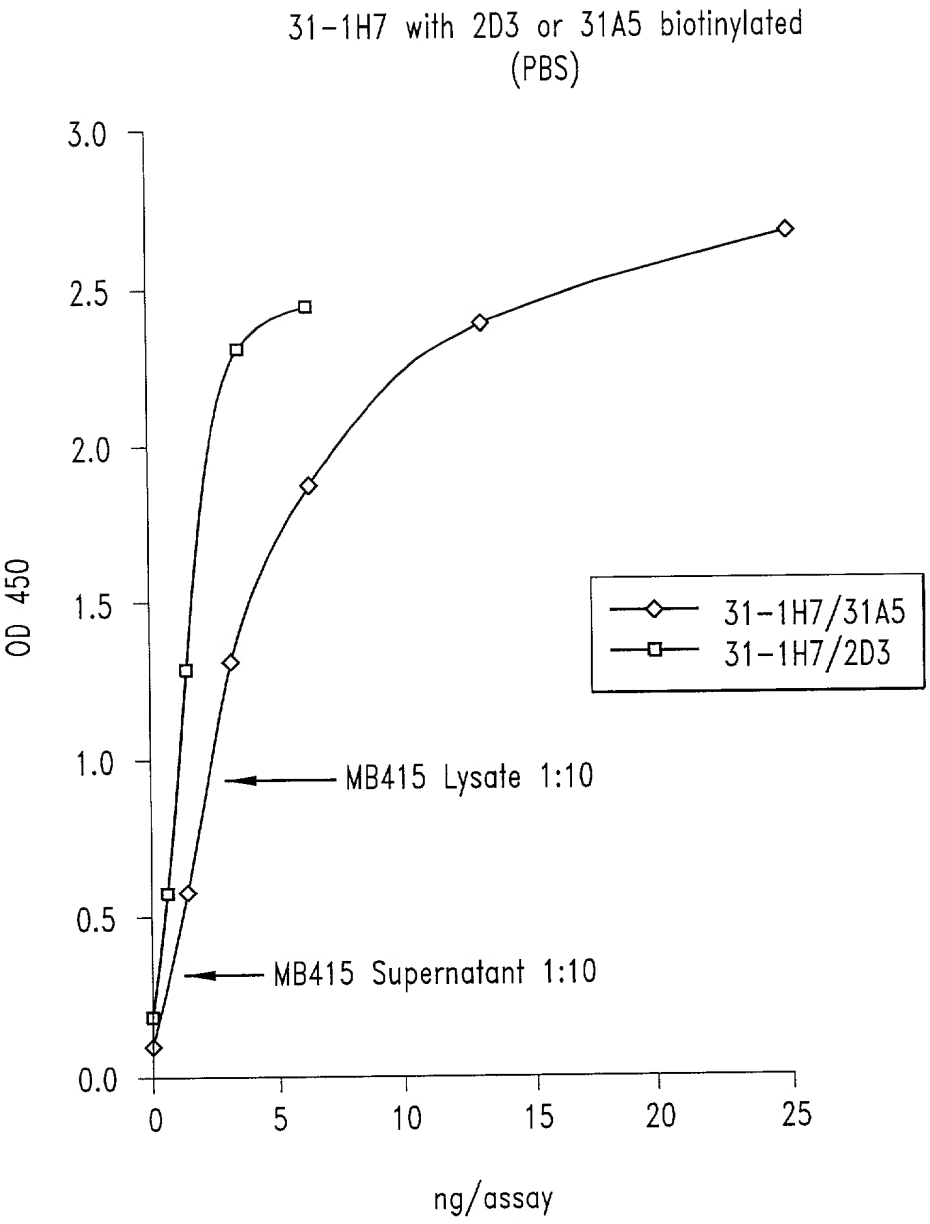

31-1H7 with 2D3 or 31A5 biotinylated
(PBS)
OD 450
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0
5
10
15
20
25
ng/assay
31-1H7/31A5
31-1H7/2D3
MB415 Lysate 1:10
MB415 Supernatant 1:10

Fig. 7C

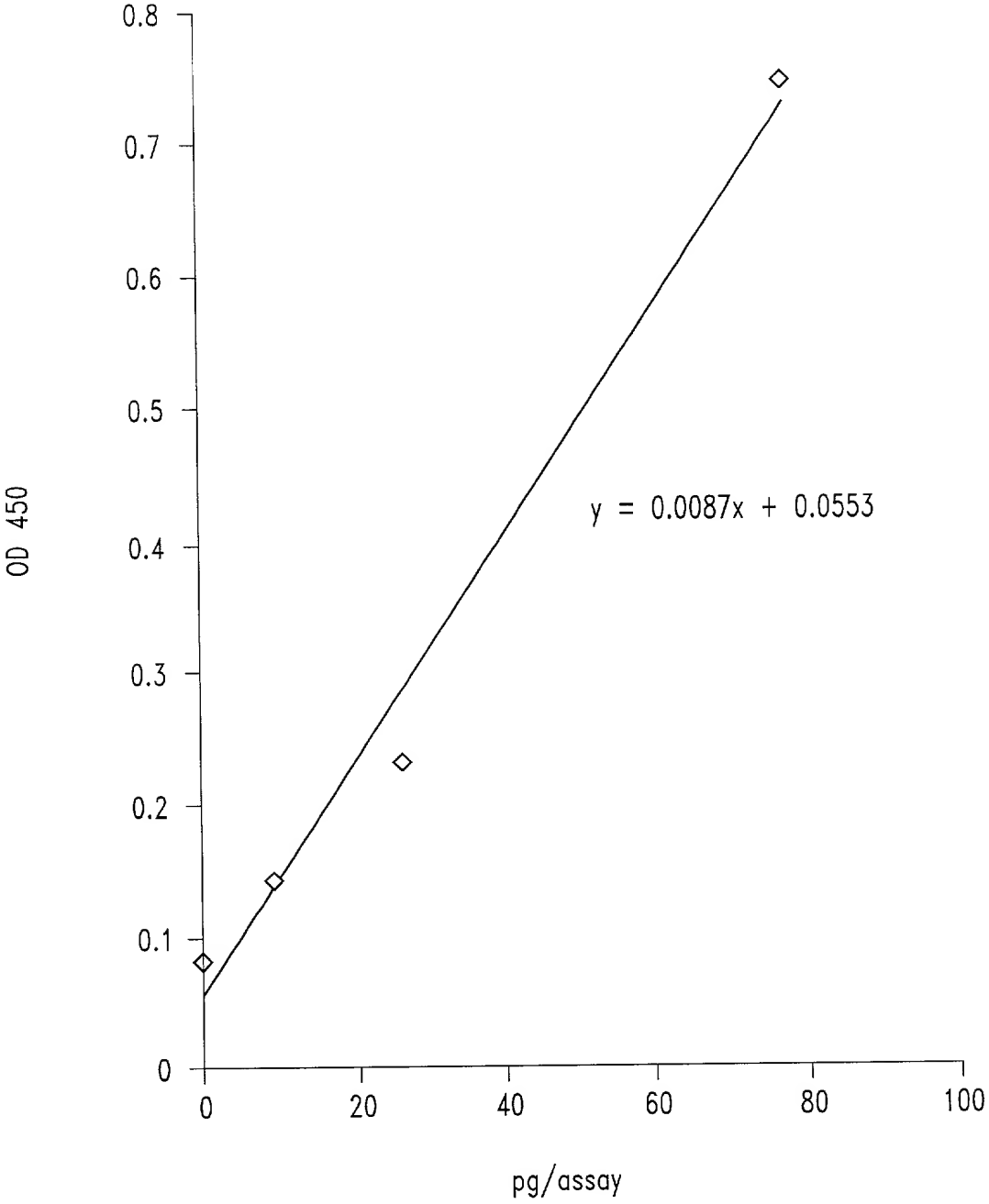

0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
OD 450
y = 0.0087x + 0.0553
0
20
40
60
80
100
pg/assay

Fig. 8

Detection of mmamglobin in sera

Serum #	Status	Western	Sandwich ELISA 2D3 mAb capture, 29C11 secondary		Sandwich ELISA 967 Ab capture, 2D3 mAb secondary	
			Mammaglobin [pg/ml]	OD	Mammaglobin [pg/ml]**	MRNA in blood*
6 (aka 3534)	BrCA	+	4980-9600	3 8	8732	not tested
3	BrCA	nd	560-1245	2.6	2392	+
4	BrCA	nd	311-622	1.7	1443	+
12	BrCA	nd	311-622	1.5	2298	weakly +
17	BrCA	nd	149-311	0.6	1498	+
11	BrCA	nd	149-311	0.6	847	+
10	BrCA	nd	74-149	0 38	356	nd
1	Normal F	nd	38-74	0.21	2333	not tested
18	Normal M	nd	38-74	0.2	636	not tested
8	BrCA	nd	38-74	0.19	284	nd
9	Normal F	nd	38-74	0.18	188	not tested
5	Normal F	nd	<33	0.16	43	not tested
2	Normal F	nd	<33	0.14	149	not tested
7	Normal F	nd	<33	0.13	96	not tested
14	Normal F	nd	<17	0.05	18	not tested
16	Normal F	nd	<17	0.01	363	not tested
13	Normal F	nd	<17	0.01	443	not tested
15	Normal F	nd	xxx	xxx	10.8	not tested

Fig. 9

1a MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

2a MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

3a MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

4a MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

5a MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

6a MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

7a MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

8a MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

peptide #	AA sequence	AA location within mmgb
1a	MKLLMVLMLAALSQHCYAGS	1-20
2a	ALSQHCYAGSGCPLLENVIS	11-30
3a	GCPLLENVISKTINPQVSKT	21-40
4a	KTINPQVSKTEYKELLQEFI	31-50
5a	EYKELLQEFIDDNATTNAID	41-60
6a	DDNATTNAIDELKECFLNQT	51-70
7a	ELKECFLNQTDETLSNVEVF	61-80
8a	DETLSNVEVFMQLIYDSSLCDLF	71-93

Fig. 10

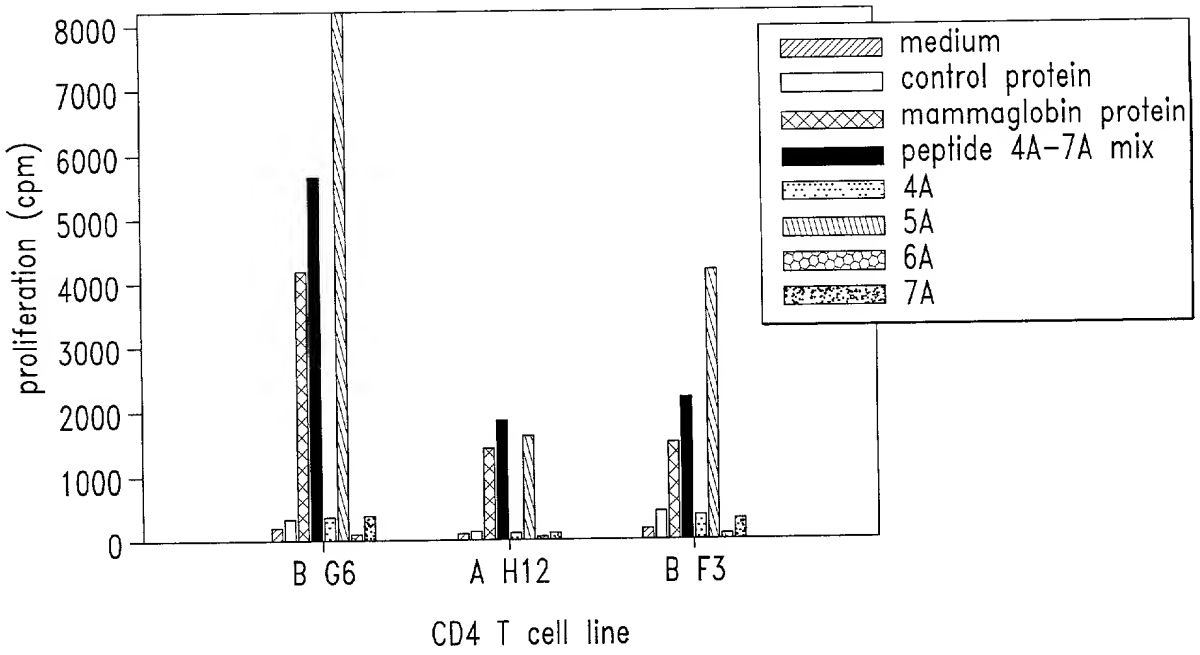


Fig. 11A

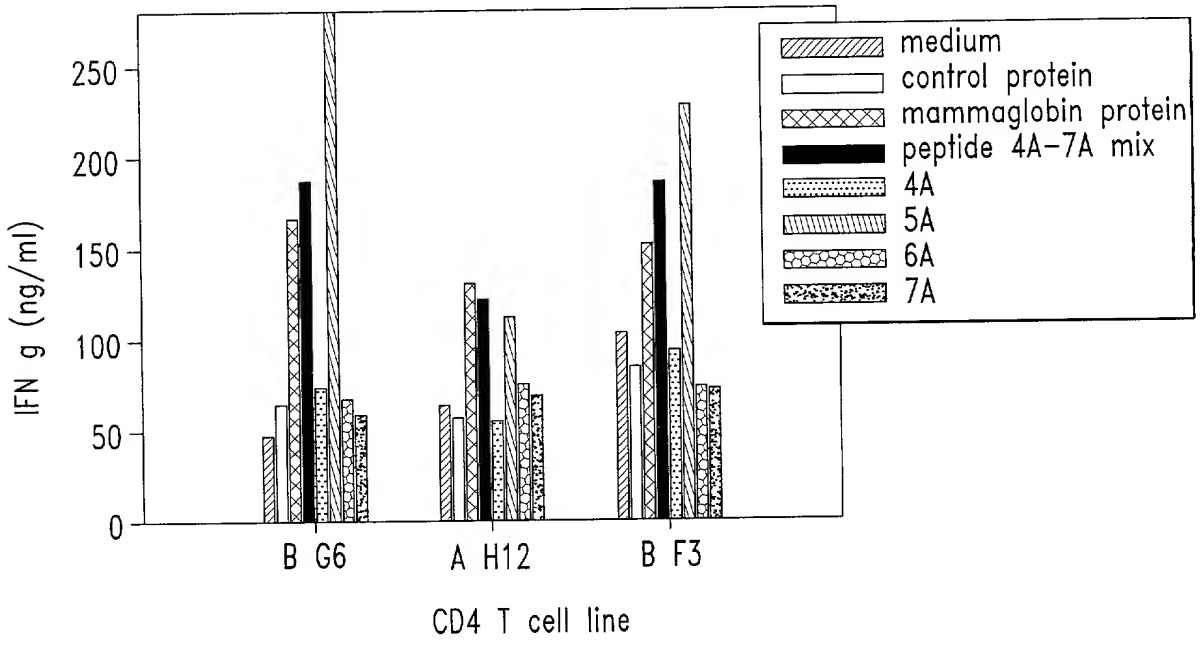


Fig. 11B

MKLLMVLMLAALSQHCYAGSGCPLLENVISKTINPQVSKTEYKELLQEFIDDNATTNAIDELKECFLNQTDETLSNVEVFMQLIYDSSLCDLF

#	Start positon	sequence (length)	score
1	2	KLLMVLMLA (9)	148
2	3	LLMVLMLAA (9)	72
3	4	LMVLMLAAL (9)	60
4	66	FLNQTDETL (9)	48
6	83	LIYDsSLCDL (10)	151
7	2	KLLMvLMLAA (10)	148
8	80	FMQLiYDSSL (10)	71
9	58	AIDEiKECFL (10)	26
10	45	LLQEfIDDNA (10)	17

Fig. 12

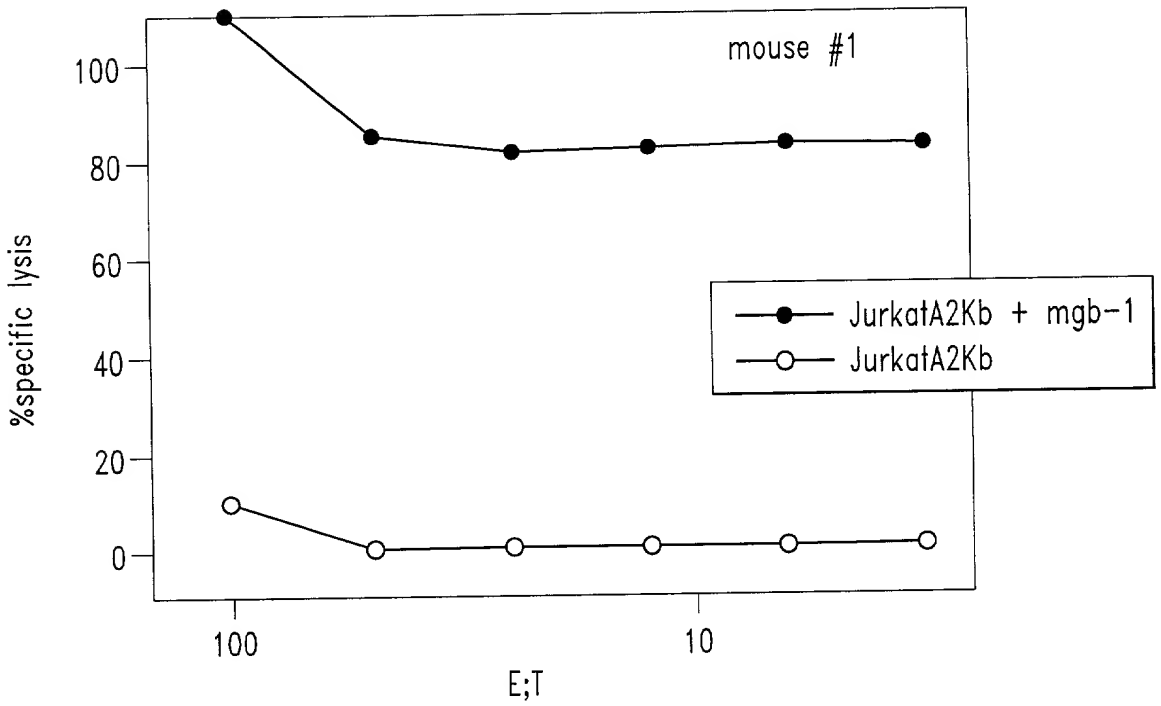


Fig. 13A

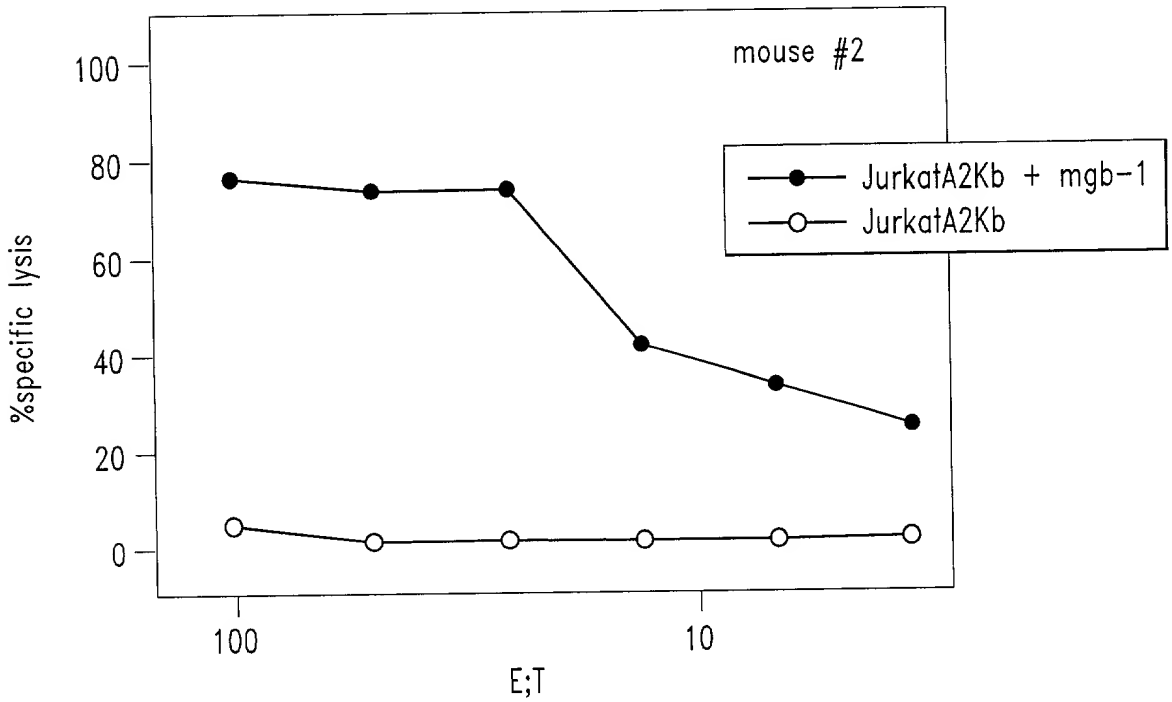


Fig. 13B

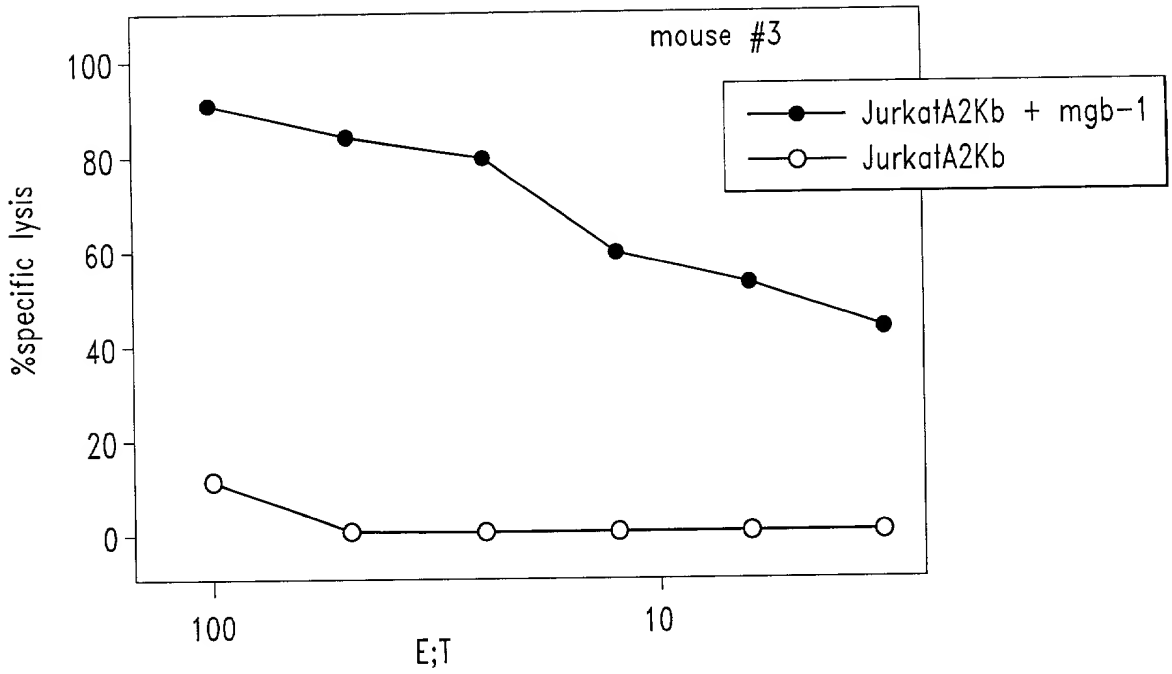


Fig. 13C

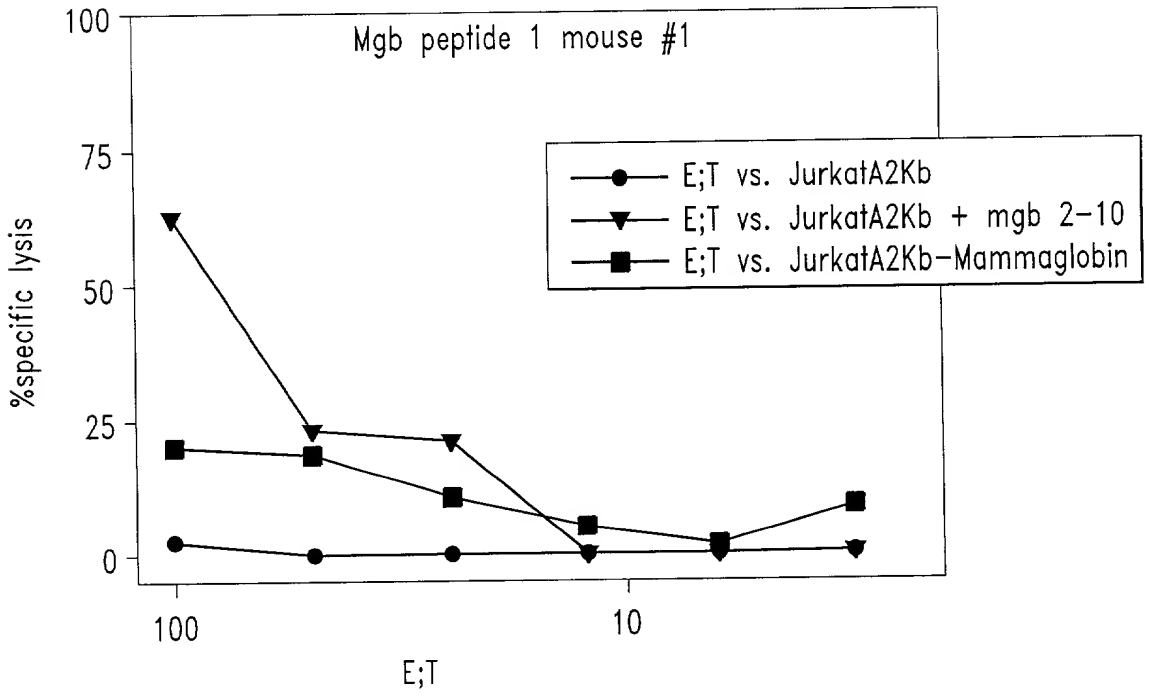


Fig. 14A

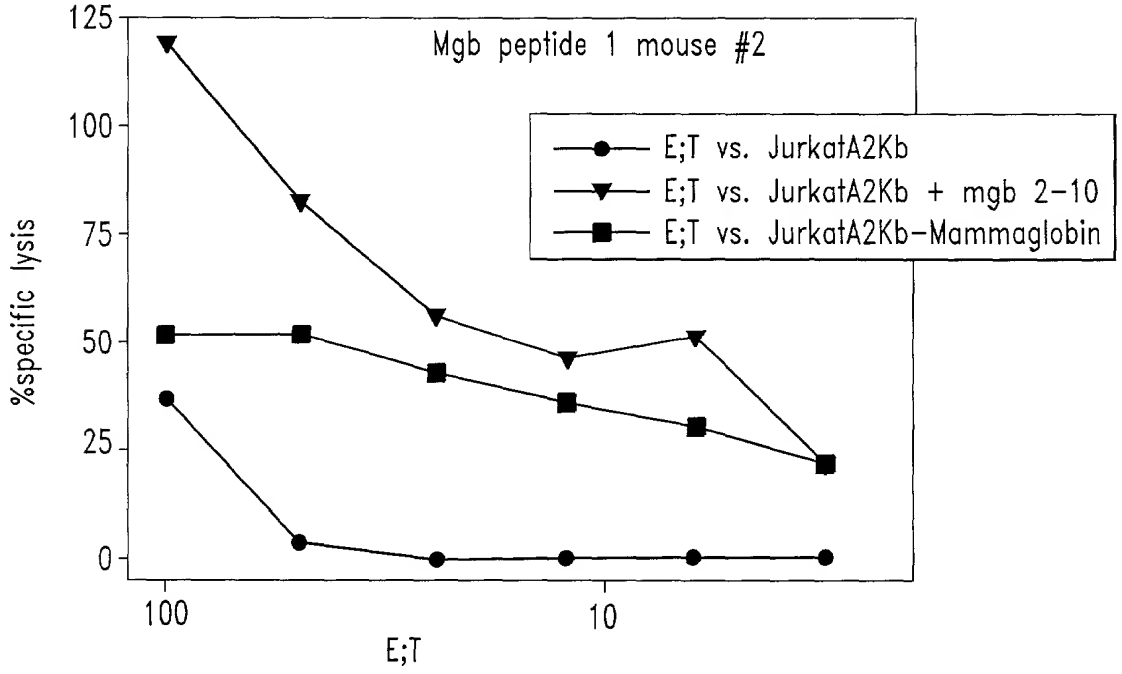


Fig. 14B

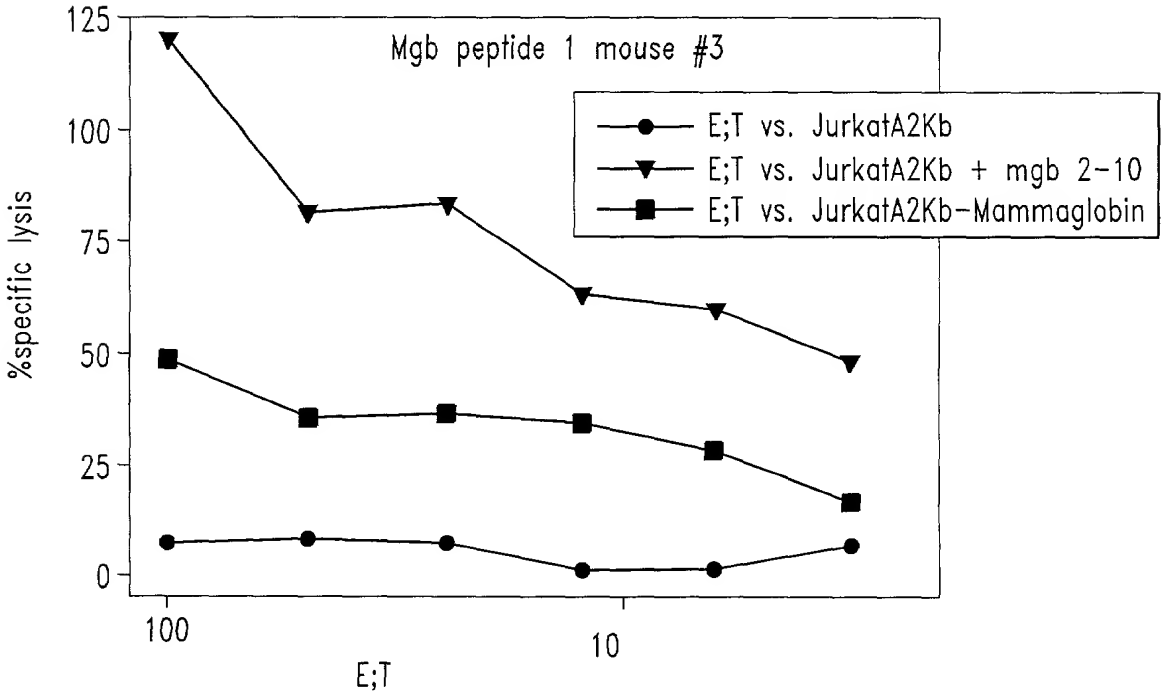


Fig. 14C

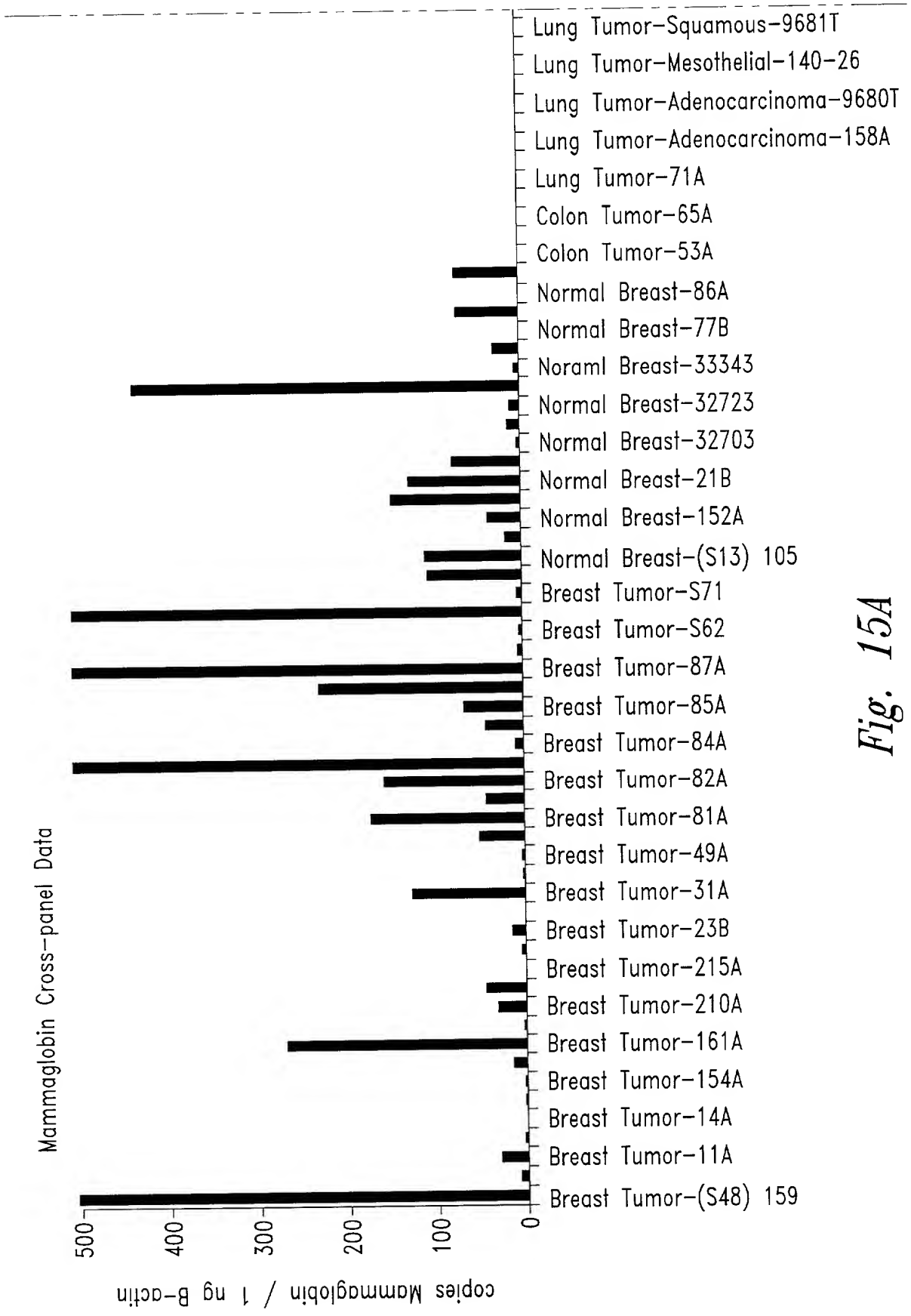

Mammaglobin Cross-panel Data
copies Mammaglobin / 1 ng B-actin
0
100
200
300
400
500
Lung Tumor-Squamous-9681T
Lung Tumor-Mesothelial-140-26
Lung Tumor-Adenocarcinoma-9680T
Lung Tumor-Adenocarcinoma-158A
Lung Tumor-71A
Colon Tumor-65A
Colon Tumor-53A
Normal Breast-86A
Normal Breast-77B
Noraml Breast-33343
Normal Breast-32723
Normal Breast-32703
Normal Breast-21B
Normal Breast-152A
Normal Breast-(S13) 105
Breast Tumor-S71
Breast Tumor-S62
Breast Tumor-87A
Breast Tumor-85A
Breast Tumor-84A
Breast Tumor-82A
Breast Tumor-81A
Breast Tumor-49A
Breast Tumor-31A
Breast Tumor-23B
Breast Tumor-215A
Breast Tumor-210A
Breast Tumor-161A
Breast Tumor-154A
Breast Tumor-14A
Breast Tumor-11A
Breast Tumor-(S48) 159

Fig. 15A

Normal Testes-4C
Normal Stomach-73A
Normal Stomach-137A
Normal Stomach-137A
Normal Small Intestine-66B
Normal Skin-138A
Normal Skin-60A
Normal Skeletal Muscel-128A
Normal Retina-32263
Normal Ovary-93B
Normal Lung-Clontech
Normal Lung-58A
Normal Lung-51C
Normal Liver-56A
Normal Liver-136A
Nomal Kidney-69A
Normal Kidney-119A
Normal Esophagus-1375
Normal Colon-50B
Normal Brain-Clontech
Normal Brain-75A
Normal Bone Marrow-74A
Normal Bladder-S9-1
Normal Aorta-1375
Normal Prostate-131A
Normal Prostate-48B
Normal Prostate-45A
Normal Prostate-34C
Normal Prostate-117A
Prostate Tumor-40A
Prostate Tumor-35A
Prostate Tumor-135A
Prostate Tumor-115A
Ovary Tumor-120A
Lung Tumor-Squamous-96A

Fig. 15B

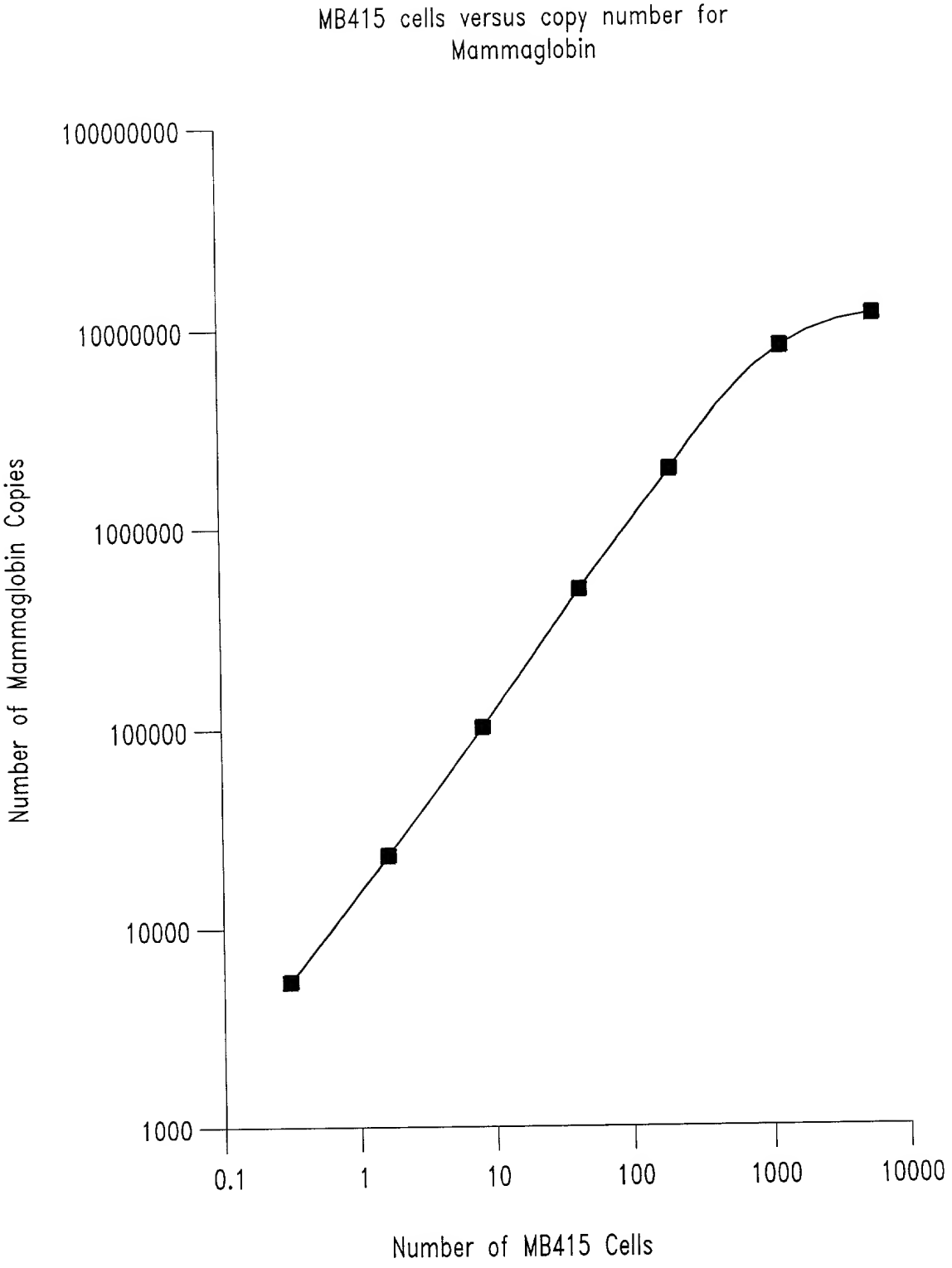

MB415 cells versus copy number for Mammaglobin
100000000
10000000
1000000
100000
10000
1000
Number of Mammaglobin Copies
0.1
1
10
100
1000
10000
Number of MB415 Cells

Fig. 16

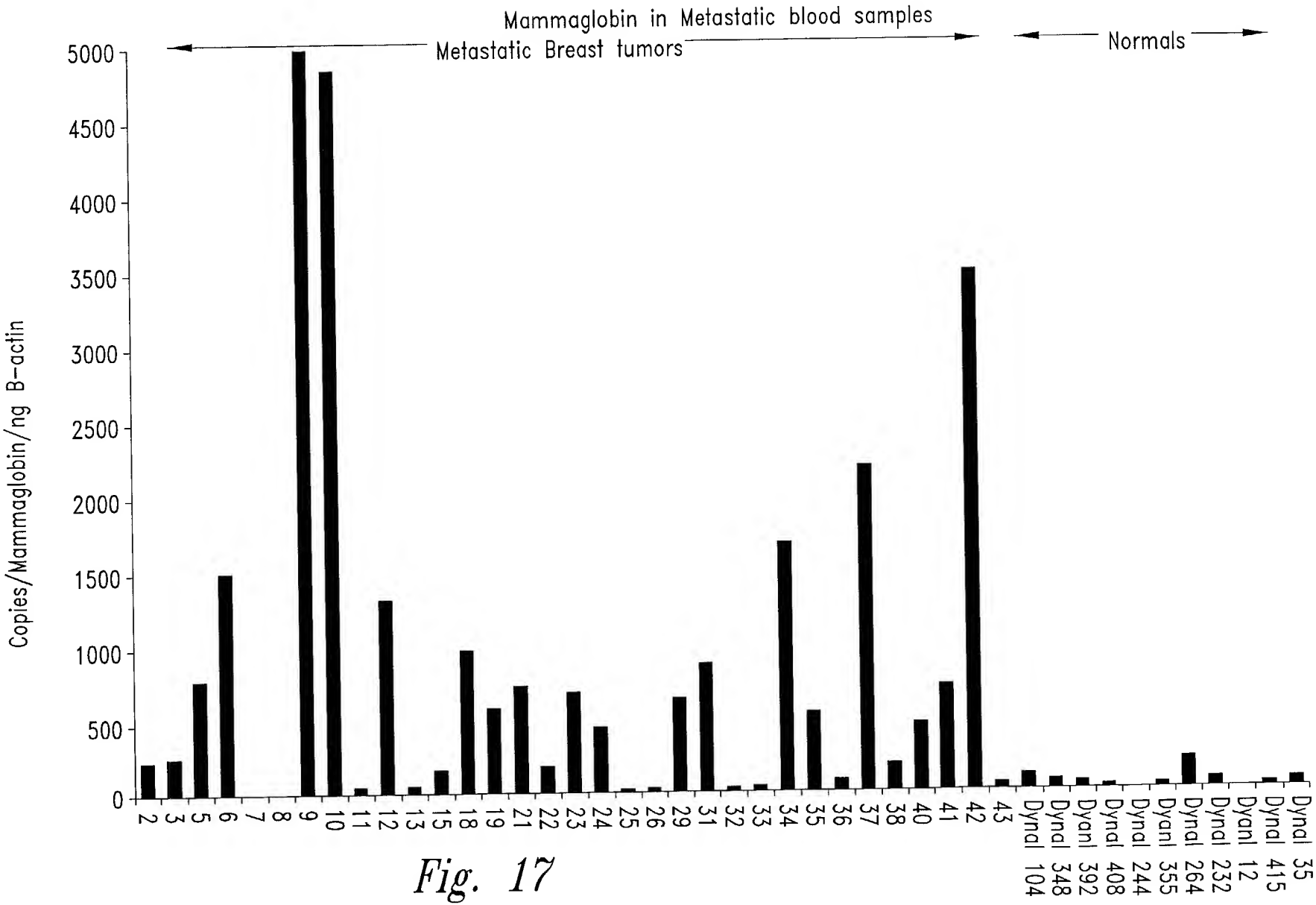

Mammaglobin in Metastatic blood samples
Metastatic Breast tumors
Normals
Copies/Mammaglobin/ng B-actin
5000
4500
4000
3500
3000
2500
2000
1500
1000
500
0
2
3
5
6
7
8
9
10
11
12
13
15
18
19
21
22
23
24
25
26
29
31
32
33
34
35
36
37
38
40
41
42
43
Dynal 104
Dynal 348
Dynal 392
Dynal 408
Dynal 244
Dynal 355
Dynal 264
Dynal 232
Dynal 12
Dynal 415
Dynal 35

Fig. 17

FIGURE 18

D117 mgb CD4 proliferation - large assay #2

line #	name	priming pep	media	DMSO	1A-7A	3A	5A	7A	mgb B 5A	Hmamm 10	Hmamm 1	Hmamm .1
1	AB:C9	5A	551	549	5478	454	12599	329	886	5989	1944	1222
2	AB:C11	5A	155	84	13737	159	17250	137	596	18027	14327	4599
3	AB:E7	5A	582	551	7815	198	12876	465	1264	11457	8696	1890
4	AB:H12	5A	1309	1725	18113	965	5850	1264	295	1159	4232	922
5	AB:A7	1A-7A	588	683	15646	4500	112	22045	417	2758	1922	792
6	AB:A9	1A-7A	478	376	6939	396	426	4095	135	416	282	135
7	AB:B9	1A-7A	1802	1802	29047	9277	2828	5838	1177	617	883	2307
8	AB:C9	1A-7A	2142	2258	16814	3158	2836	11635	2954	925	1006	790
9	AB:G7	1A-7A	1553	992	7754	2004	3155	3829	492	5405	3744	2524
10	AB:G9	1A-7A	1607	1577	7583	1489	3487	1752	689	5639	2586	2288
11	AB:H12	1A-7A	3101	2529	23408	24070	2984	8379	2953	15009	5988	2759
12	AB:H4	1A-7A	878	891	16769	674	3658	11797	478	1157	1169	667
13	CD:A4	1A-7A	124	520	20866	21642	805	3049	167	16009	4096	455
14	CD:A5	1A-7A	1439	328	12841	22252	2925	1358	563	4822	883	211
15	CD:C7	1A-7A	76	48	67	86	39	38	40	106	91	79
16	AB:G7	5A	173	477	1073	184	127	489	562	985	543	629
17	AB:H12	5A	948	329	2001	849	1301	266	380	775	1340	355
18	AB:C10	5A	223	181	486	254	341	97	204	340	252	133
19	AB:C11	5A	247	164	22726	148	15534	161	222	20054	21793	8331
20	AB:G6	5A	2125	2048	2408	1618	985	1496	1217	4175	2548	1645
21	AB:G7	5A	91	167	1689	162	2582	93	70	1013	516	178
22	AB:H2	5A	411	720	21053	271	11029	157	220	10420	9317	6009
23	AB:D1	5A	222	608	204	412	276	125	57	1991	1171	741
24	AB:E9	5A	315	457	390	191	1195	177	135	647	286	341
25	AB:G6	1A-7A	485	295	5014	70	2148	48	455	20516	12078	5873
26	AB:H4	1A-7A	545	192	14133	190	891	7519	105	2647	969	578
27	AB:D12	1A-7A	1652	1522	13318	6496	3131	4081	946	20077	11118	8972
28	AB:D1	1A-7A	1448	1614	4205	1199	1186	1822	430	5215	3124	3258
29	AB:H1	1A-7A	5572	3885	18628	14527	1817	13029	1587	11289	4834	1966
30	AB:A7	1A-7A	1072	525	15470	2718	907	12379	280	5261	2080	359
31	AB:B12	1A-7A	540	797	17558	703	15480	659	6354	18054	13983	5575
32	AB:F7	1A-7A	551	455	8374	7694	2462	329	996	2681	2532	941
33	AB:G7	1A-7A	652	710	8278	1018	3753	2941	624	6170	3583	1050
34	CD:C7	1A-7A	109	175	14322	3891	10183	628	76	9439	2217	976
35	CD:D8	1A-7A	824	2270	10295	4280	1691	1314	997	1715	761	710
36	CD:G4	1A-7A	177	72	29912	97	24392	103	54	18285	13873	10861
37	CD:G5	1A-7A	230	152	16874	161	6497	45	103	15209	9892	4354
38	CD:G3	1A-7A	146	178	26356	138	22005	90	96	19894	15188	10128
39	CD:G6	1A-7A	129	84	12775	115	2504	91	80	6922	3365	696
40	CD:C9	1A-7A	2293	2507	8808	3372	2634	3247	2610	3722	2296	1937
41	CD:H10	1A-7A	430	290	29772	306	23992	498	424	20508	22871	7906
42	CD:H11	1A-7A	542	227	24760	324	17835	128	131	16142	15562	10109

FIGURE 19

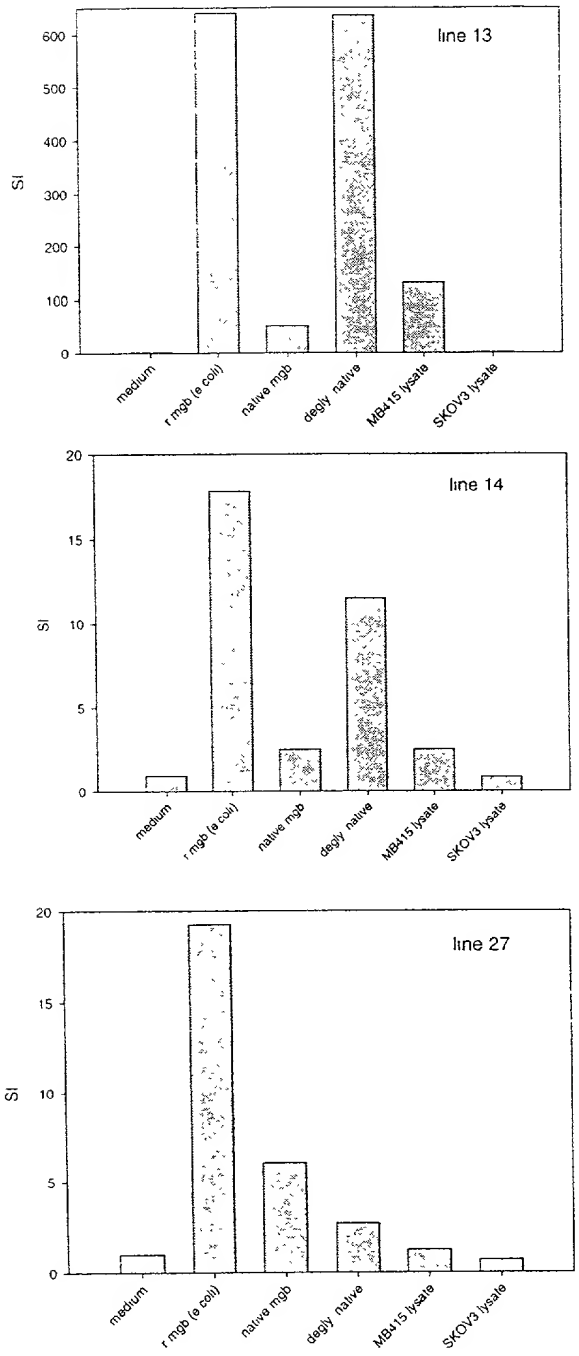

line 13
SI
600
500
400
300
200
100
0
medium
r mgb (e coli)
native mgb
degly native
MB415 lysate
SKOV3 lysate
line 14
SI
20
15
10
5
0
medium
r mgb (e coli)
native mgb
degly native
MB415 lysate
SKOV3 lysate
line 27
SI
20
15
10
5
0
medium
r mgb (e coli)
native mgb
degly native
MB415 lysate
SKOV3 lysate

Fig. 20

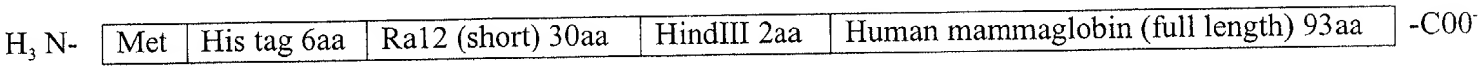
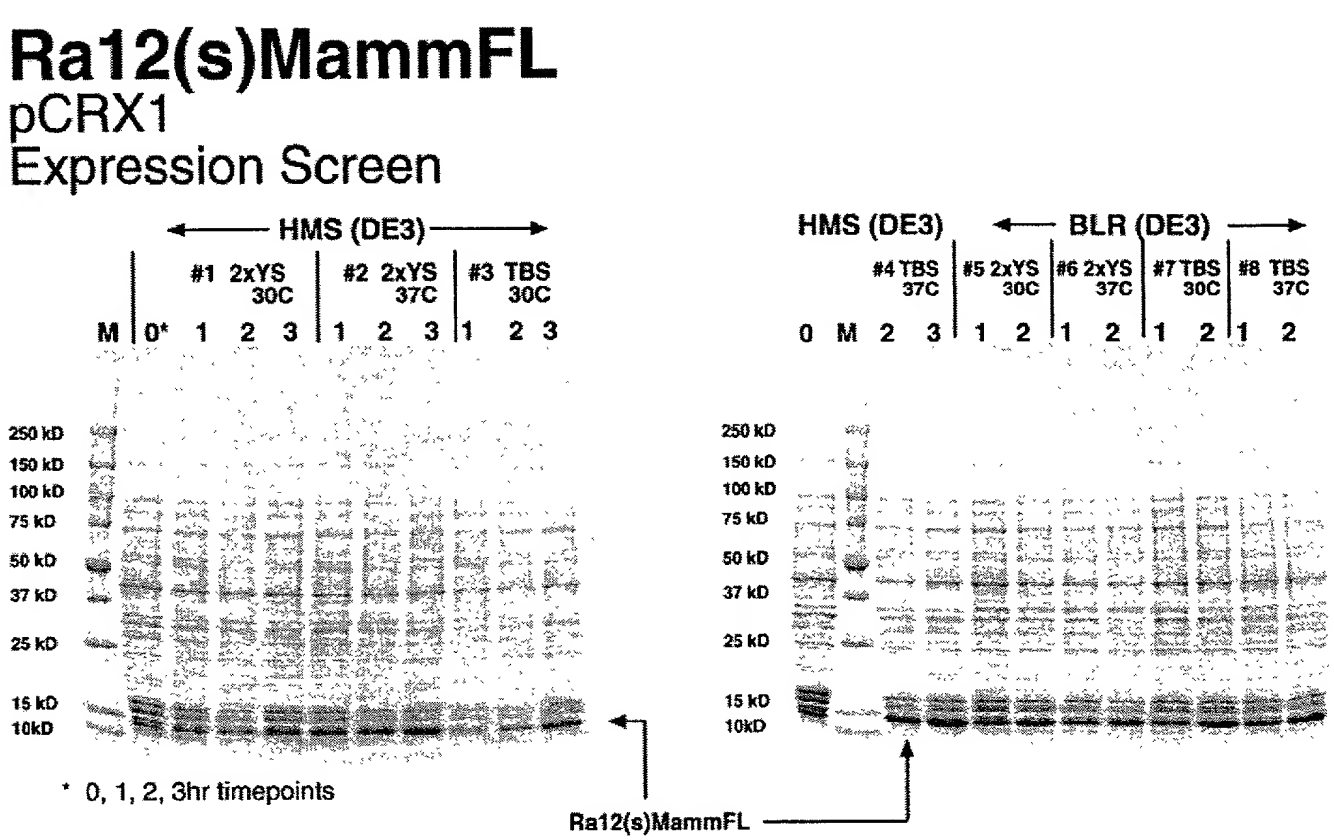


FIGURE 21


Ra12(s)MammFL
pCRX1
Expression Screen
HMS (DE3)
#1 2xYS 30C
#2 2xYS 37C
#3 TBS 30C
M 0* 1 2 3 1 2 3 1 2 3
250 kD
150 kD
100 kD
75 kD
50 kD
37 kD
25 kD
15 kD
10kD
* 0, 1, 2, 3hr timepoints
HMS (DE3)
BLR (DE3)
#4 TBS 37C
#5 2xYS 30C
#6 2xYS 37C
#7 TBS 30C
#8 TBS 37C
0 M 2 3 1 2 1 2 1 2 1 2
Ra12(s)MammFL